



FIG. I

IG-LIKE

M NR1	MSSSCSGLTRVLVAVATALVSSS
M IL-6R	MLTVGCTLLVALLAAPAVALLVLS
H CNTFR	MAAPVPWACCAVLAAA
H IL-12p40	MCHQQLVISWESLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDG
M GM-CSFR	MTSSHAMNITPLAQLALLFSTLLIPGTO

M NR1	-VDWFERDGSRLLOQ	-----	PDSGLGHRLLVLAQVDS	SPCEGTXXVCQTLDGVSGGMVT
M IL-6R	VTIHWVYSGSONR	-----	EWTGNTLVLRDVQLSDTGDXLCSLNDHLVGTVP	LL
H CNTFR	--VTWRVNGTDLA	-----	PDLNGSQLVLHGLELGHSGLXACFHRDSWHLRHQ	VL
H IL-12p40	--ITWTLDOSSSEV	-----	LGSGKTLTIQVKEFGDAGQXTCHKGGEVLSHSL	LL
M GM-CSFR	--LTWACDTAAGNVTVT	-----	SCTVTSREAGIHRRVSPFGCRCWFRMMALHHGVT	LDVNGT

M NR1	LKLG	-----
M IL-6R	VDV	-----
H CNTFR	LHVGL	-----
H IL-12p40	LHKKEDGIWSTDILKDQKE	
M GM-CSFR	VGGAAAHWRLLS-FVNESAA	

A-----A

FIG. 2A

A

A

M NR1
M IL-6R
H CNTFR
H IL-12p40
M GM-CSFR

SD100A

PPARPEVSCQAVDX-EMFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWP
PPEEPKLSCFRKNPLVMAICEWRPSSPTSPPTTKAVLFAKKINTNGK-----SDFQVP
PPREPVLSCRSNTXPKGFYCSWHLPTPTYPNTFNVTVLH-----GSKIMV
PKNKTFLRCEAKNYSGRFTCWLTTI-----STDLTFSVKSSRGSS-----DPQGV
GSGAENLTCEIRAA-RFLSCAWREGPAA--PADVRYSLRVLNST-----GHDVAR

M NR1
M IL-6R
H CNTFR
H IL-12p40
M GM-CSFR

CPQDPLE-----ASRCVVHG-----AELWSEYRTNVTEVNPL--GASTCLLD
CQYSQQLK-----SFSCQVE-----ILEGDKVYHIVSLCVANSVGSKSSHNE
CEKDPAL-----KNRCHIRYMHFLFTIKYKVISVSNAL-----GHNATAIT
CGAATLSAERVRGDNKEYEYSEVCEQEDSACPAAKESLPFVMDAV--HKLKYENYTS
CMADPGDDV-----ITQCIA-----NDLSLLGSEAYLVVTGRSGAGPVRFLDD

M NR1
M IL-6R
H CNTFR
H IL-12p40
M GM-CSFR

VRLOSTLR---
AFHSLKMQVQ--
FDEFTIVK---
FFIRDIK---
VVATKALERLG

B

B

FIG.2B

B

M NR1 PDPPQGLRVESVPGYPRRLHGSWTYPASWPRQPHFL-----LKLRLQXRPAQHPAWSTV
M IL-6R PDPPANLVVSAIPGRPRWLKVSQHPETWDPY-YL-----LQFQLRXPVWSKEFTVL
H CNTFR PDPPENVVARPVPSNPRRLEVITWQTPSTWDPDESFLKFF-LRYRPLILDQWQHVELSD
H IL-12p40 PDPPNNLQLK-PLKNSRQVEVSWEXPDWTSTPHSYFSLTFCVQVQGKSREKKDRVFTD
M GM-CSFR --PPRDVT---ASCNSSHCTVSWAPPSTWASLTARDFQFE-VQWQSAEPGSTPRKVLVV

SD100B

M NR1 RPIGL--EEVITDAVAGLPMVRVSARDFLDAGTWSAWSPEAWGTPSTG-PLQDEIPD-
M IL-6R LLPVAQYQCVIHDAIRGVKMVVQVRGKEELDGLQWSEWSPEVTGTPWIAEPRTTPAGIL
H CNTFR GT-----AHTITDAYAGKEYIIQVAAKDNEI-GTWSWVAHAHATPWTEPRHLTTEAQ
H IL-12p40 KT-----SATVICRKNASISVRAQDRYYSSSWSEWASVPCS*
M GM-CSFR KETRL----AFPSAPHGGMKVVRAGDTRMK-HWGEWSPAHL-EAEDTRVP-----

M NR1 WSQGHGQQLVVVAQEDSPAPARPSLQDPRPLDHRDPLEQ
M IL-6R WNPTQSVEDSANHEDQYESSTEATSVLAPVQESSMSLPT
H CNTFR AAETTTSTTSSSLAPPPTTKIC-----
M GM-CSF -----

M NR1 VAVLASLLGIFSCGLGAVGALALGLWLRLRRSGKDGPKGLLA--PMIPVEKLPGIPN
M IL-6R FLVAGGSLAFGLLLCVFIIL-----RLKQWKSEAEKESKTTSPPPPYSGLPLKPT
H CNTFR DPGELSGGGPSAPFLVSVPI TLALAAAAATASSLLI*
M GM-CSF ALLYAVTACAVLLCALALGVTC-----RRFEVTR-----LYPPPIGIRD

TM/CYT

M NR1 LQRTPENFS*
M IL-6R FLLVPLLTPHSSGSDNTVNHSCLGVRDAQSPYDNSNRDYLFPF*
M GM-CSFR KVSDDVRVNPETLRKDLLQP*

C

FIG.2C

TCTAACAGCC	TTACCCCACT	TGGTGCATCA	ATTTTCTCC	TAGGAAGCCT	CAGTTTGGG	60
GAGGAAGAGC	CAGGCTTTAG	CTCCCATCTC	AGGGTCGGG	GATTTTGGAC	TCTACCTCTC	120
CCCACAG	ATG AGC AGC	TGC TCA GGG	CTG AGC AGG	GTC CTG GTG	GCC	169
Met Ser Ser	Cys Ser Cys	Gly Ser Gly	Leu Ser Arg	Val Leu Val	Ala	
1	5	10				
GTG GCT ACA	GCC CTG GTG	TCT GCC TCC	TCC CCC TGC	CCC CAG	GCC TGG	217
Val Ala Thr	Ala Leu Val	Ser Ala Ser	Pro Cys Pro	Gln Ala	Trp	
15	20	25	30			
GGC CCC CCA	GGG GTC CAG	TAT GGG CAG	CCA GGC AGG	TCC GTG	AAG CTG	265
Gly Pro Pro	Gly Val Gln	Tyr Gly Gln	Pro Gly Arg	Ser Val	Lys Leu	
35	40	45				
TGT TGT CCT	GGA GTG ACT	GCC GGG GAC	CCA GTG TCC	TGG TTT	CGG GAT	313
Cys Cys Pro	Gly Val Thr	Ala Gly Asp	Pro Val Ser	Trp Phe	Arg Asp	
50	55	60				
GGG GAG CCA	AAG CTG CTC	CAG GGA CCT	GAC TCT GGG	CTA GGG	CAT GAA	361
Gly Glu Pro	Lys Leu Leu	Gln Gly Pro	Asp Ser Gly	Leu Gly	His Glu	
65	70	75				
CTG GTC CTG	GCC CAG GCA	GAC AGC ACT	GAT GAG GGC	ACC TAC	ATC TGC	409
Leu Val Leu	Ala Gln Ala	Asp Ser Thr	Asp Glu Gly	Thr Tyr	Ile Cys	
80	85	90				
CAG ACC CTG	GAT GGT GCA	CTT GGG GGC	ACA GTG ACC	CTG CAG	CTG GGC	457
Gln Thr Leu	Leu Asp Gly	Ala Leu Gly	Thr Val Thr	Leu Gln	Leu Gly	
95	100	105	110			

FIG. 8A

A

A

A

TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG	505
Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu	115 120 125
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC	553
Asn Phe Ser Cys Thr 130	135 140
CGC TAC CTC ACC TCC TAC AGG AAG ACA GTC CTA GGA GCT GAT AGC	601
Arg Tyr Leu Thr Ser Tyr Arg Lys 150	155
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC	649
Gln Arg Arg Ser Pro Ser Thr Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro	160 165 170
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG	697
Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln	175 180 185 190
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA	745
Tyr Arg Ile Asn Val Thr Glu Val Val Asn Pro Leu Gly Gly Ala Ser Thr	195 200 205
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC	793
Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro	210 215 220
CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA	841
Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg	225 230 235

B

FIG.8B

B

GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu 240 245 250	889
CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser 255 260 265 270	937
ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala 275 280 285	985
GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala 290 295 300	1033
GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr 305 310 315	1081
GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln 320 325 330	1129
CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser 335 340 345 350	1177
CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln 355 360 365	1225

C

FIG.8C

C

GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG GTG Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val	1273
370 375 380	
GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CCG GGT GGG Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly	1321
385 390 395	
AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val	1369
400 405 410	
GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT Asp Arg Arg Pro Gly Ala Pro Asn Leu	1416
415 420	
CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA	1476
GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGA GCCCATTCT GTGAGACCCCT	1536
GTATTTCAAA TTGCGAGCTG AAAGGTGCTT GTACCTCTGA TTTACACCCCA GAGTTGGAGT	1596
TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG	1656
AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG	1716
TCCTTGGCTC TTGGCCCTTC CCCTTGCAGG GGTGTGTCAG GTGTGAATAA AGAGAATAAG	1776
GAAGTTCTTG GAGATTATAC TCAG	1800

D

FIG. 8D